



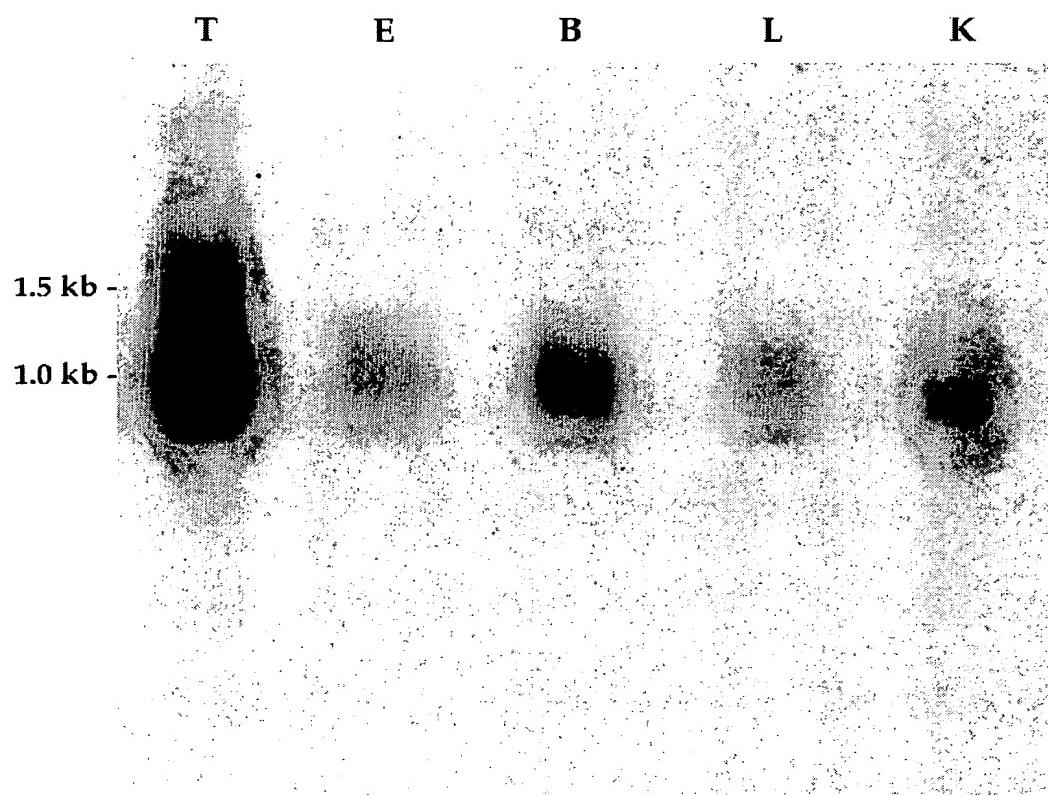
FIG. 1

SP22	MASKRALVILAKGAEEMETVI <u>PVDIMRRAGIKVTVAGLAG</u>	
1	:     :     :     :     :     :     :	40
DJ-1	MASKRALVILAKGAEEMETVI <u>PVDVMRRAGIKVTVAGLAG</u>	
	Peptide 1	
SP22	<u>KDPVQCSR</u> <u>DVVICPDTSLEEAKTQGPYDVVVLPGGNLGAQ</u>	
41	:     :     :     :     :     :     :	80
DJ-1	<u>KDPVQCSR</u> <u>DVVICPDASLEAKKEGPYDVVVLPGGNLGAQ</u>	
SP22	NLSESAV <u>KEILKEQENRKGLIAAI</u> CAGPTALLAHEVGFG	
81	:     :     :     :     :     :     :	120
DJ-1	NLSESAV <u>KEILKEQENRKGLIAAI</u> CAGPTALLAHEIGCG	
	Peptide 2	
SP22	CKVT <u>SHPLAKDKMMNGSHYSYS</u> ESRVE <u>KDGLILTSRGPGT</u>	
121	:    :     :     :   :     :     :     :	160
DJ-1	SKVT <u>THPLAKDKMMNGGHYTYS</u> ENRVE <u>KDGLILTSRGPGT</u>	
	Peptide 3 Peptide 4	
SP22	SFEFALAI <u>IVEALSGKDMANQVKAPLVLD</u>	
161	:     :   :     :     :     :	189
DJ-1	SFEFALAI <u>IVEALNGKEVAAQVKAPLVLD</u>	

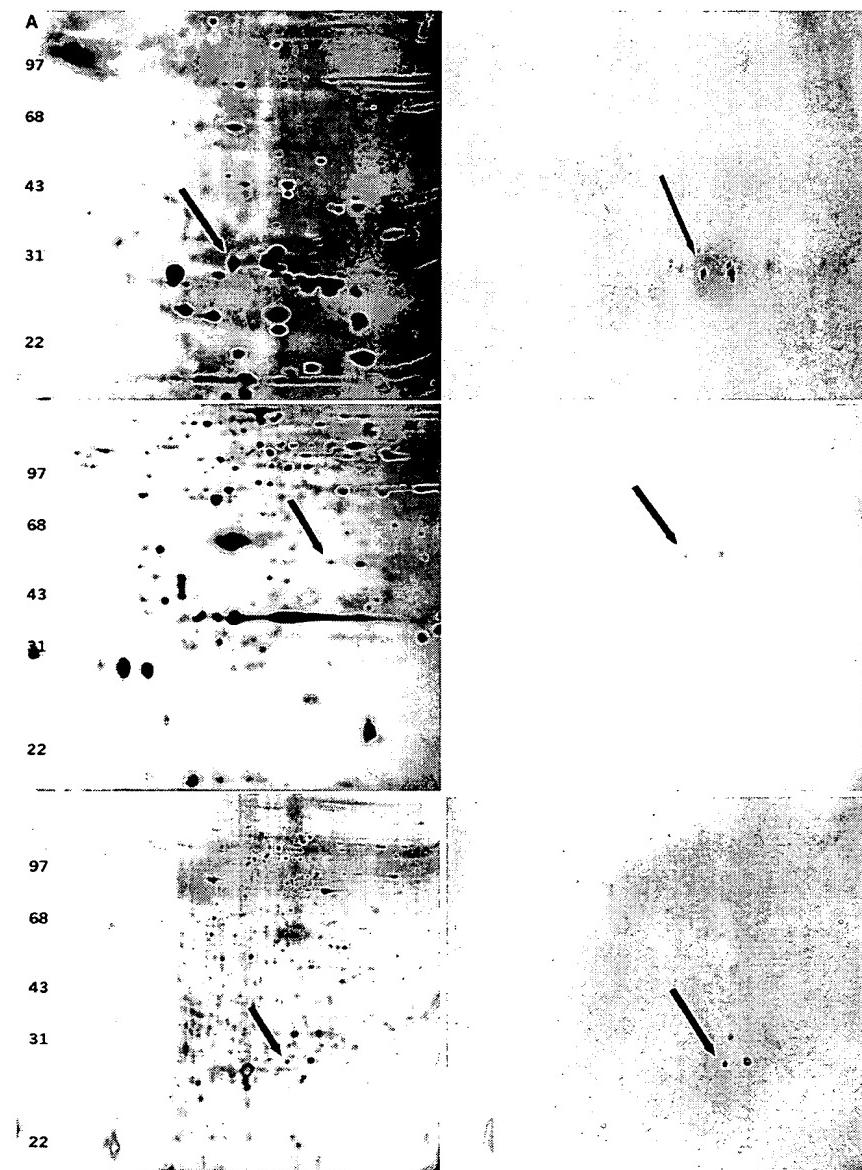
FIG. 2

1 A gctgtgcagagccgtctggcagggttacccatctttattaatcattag 65  
 66 A tagtgtggtcagagacttagcaccattgtctccccaacctggccagacattcagcagtta 130  
 131 A tcggaacagcaacaacagcaacaaaacccaaaattacaatctttaagaaatagaaATGgca 195  
 B tggcttcgcgtgggtggaggaggcgcggctcaggtctttaagaaatagaaATGgca  
 C ttgaaacctATGttqcactqtqqaqtctccacttacacacqccctattatggca  
 1 M L H C G V L H L H S L F M A 15  
 196 tccaaaagagctctggtcacccatccaaaggagcagaggagatggagacagtgattcctgtgga 260  
 16 S K R A L V I L A K G A E E M E T V I P V D 37  
 261 catcatgcggcgagctgggattaaagtccacgttcaggcttgctggagaccggccgtgcagt 325  
 38 I M R R A G I K V T V A G L A G K D P V O 58  
 Peptide 1  
 326 ttagccgtatgtatgtatccggataccagtctggagaaggcaaaaacacagggaccatac 390  
 59 C S R D V V I C P D T S L E E A K T Q G P Y 80  
 391 gatgtgggtgttccaggagggaaatctgggtgcacagaacttatctgagtcggcttggtgaa 455  
 81 D V V V L P G G N L G A Q N L S E S A L V K 102  
 456 ggagatcccaaggagcaggagaacaggaaggccatagctgcacatctgtgcgggtcctacgg 520  
 103 E I L K E Q E N R K G L I A A I C A G P T 123  
 Peptide 2  
 \*  
 521 ccctgtggctacagaagttaggcttggatgcaaggatcacatcgccaccattggctaaggacaaa 585  
 124 A L L A H E V G F G C K V T S H P L A K D K 145  
 Peptide 3  
 586 atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggccatcctcac 650  
 146 M M N G S H Y S Y S E S R V E K D G L I L T 167  
 Peptide 4  
 651 cagccgtggccctggaccagcttcgagttgcgcgtggccattgtggaggcactcagtggcaagg 715  
 168 S R G P G T S F E F A L A I V E A L S G K 188  
 716 acatggctaaccaagtgaaggccccgttctcaaagactAGagagcccaagccctggaccct 780  
 189 D M A N Q V K A P L V L K D \* 202  
 781 ggaccccccaggctgagcaggcatttggaaagcccactagagagaccacagccaggtaacctggcat 845  
 846 tggaagcccacttagtgttccacagccaggtaacctcaggaactaacgtgtgaagttagccgct 910  
 911 gctcaggaatctcgccctggctctgtactattctgagccttgcttagaataaacagttccca 975  
 976 agctc\*c\*tgacggct\* 989

**Fig. 3**



**Fig. 4**



**Fig. 5**

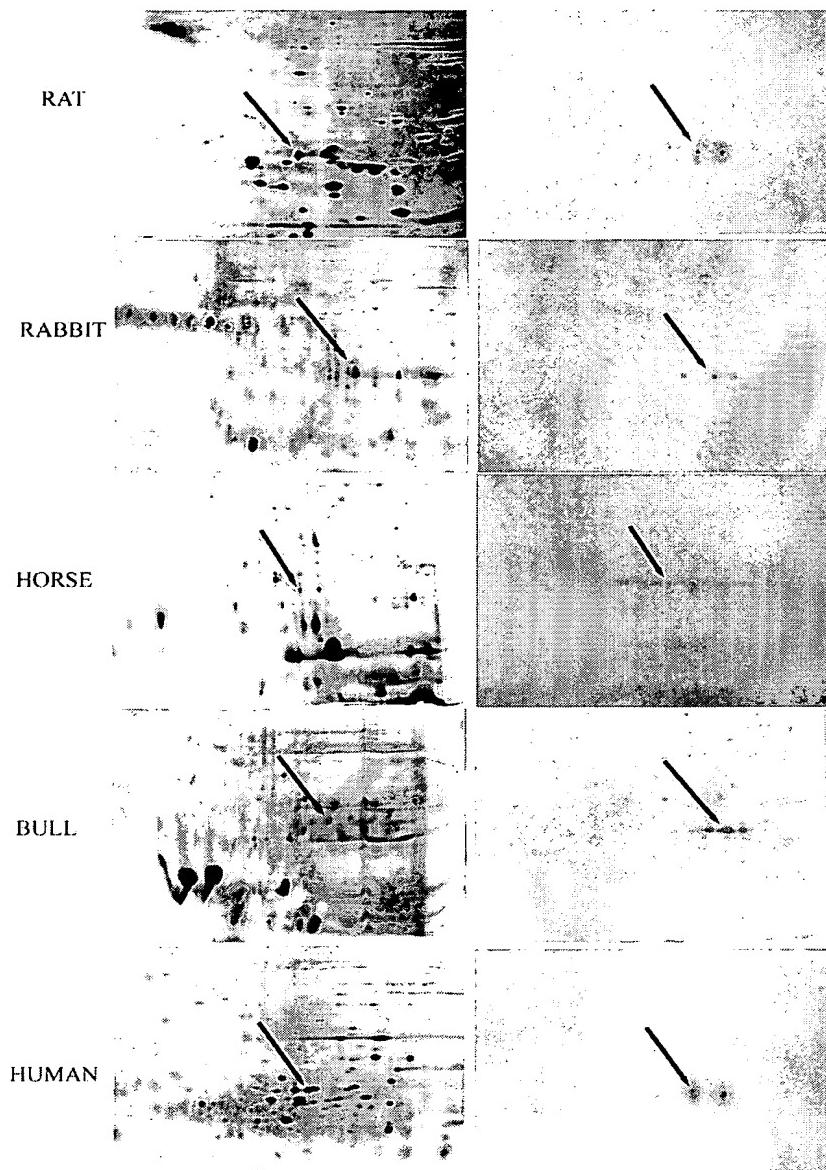
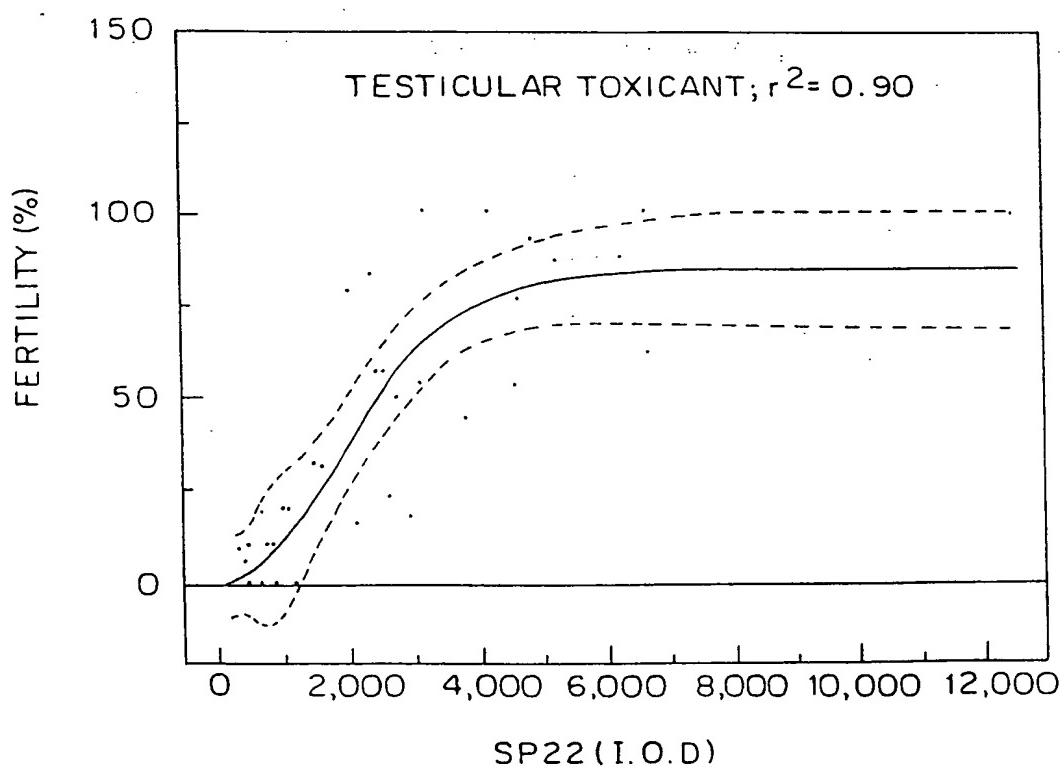
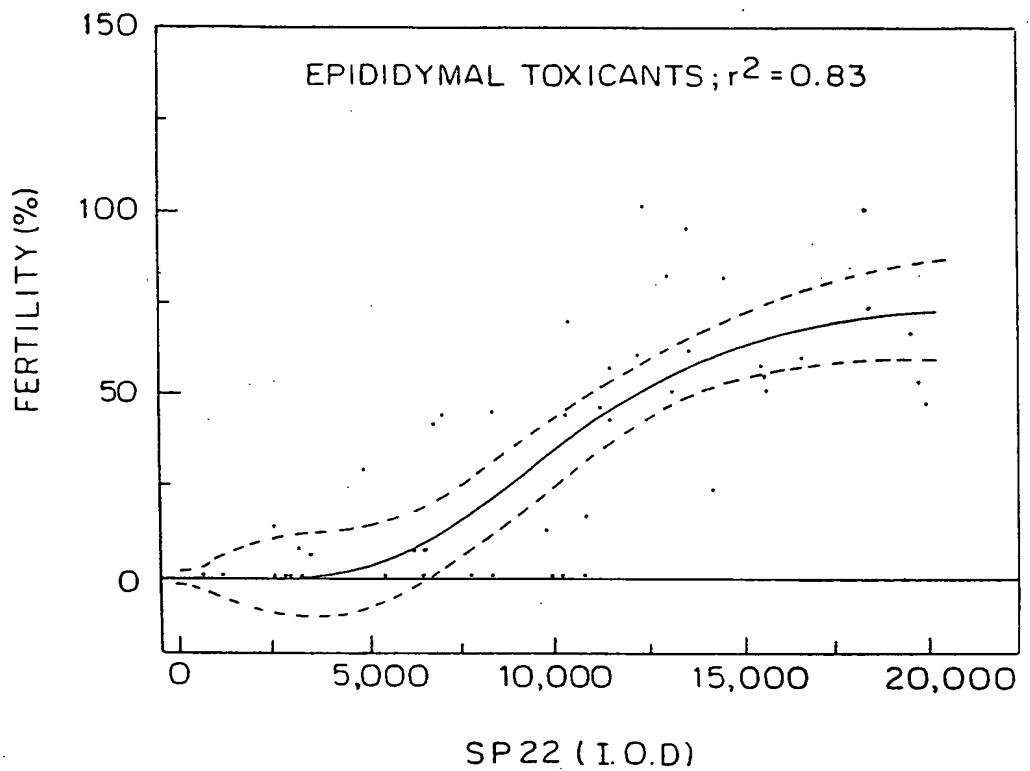


FIG. 6



150

Predictability

N = 131  
 $r^2 = 0.78$

Fertility %

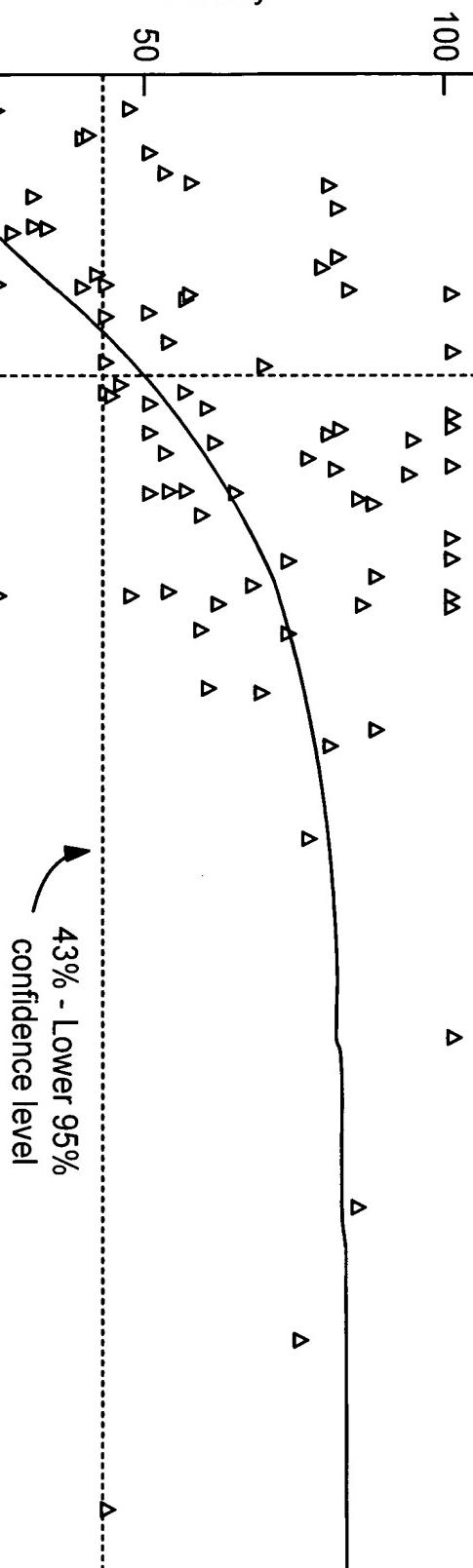
100

50

0

False Negative = 17%

True Positive = 94%



True Negative = 76%

SP22 = 3594 - Critical

SP22IOD  $\times 10^3$

FIG. 7

FIG. 8-1

FIG. 8-2

FIG. 8-3

FIG. 8

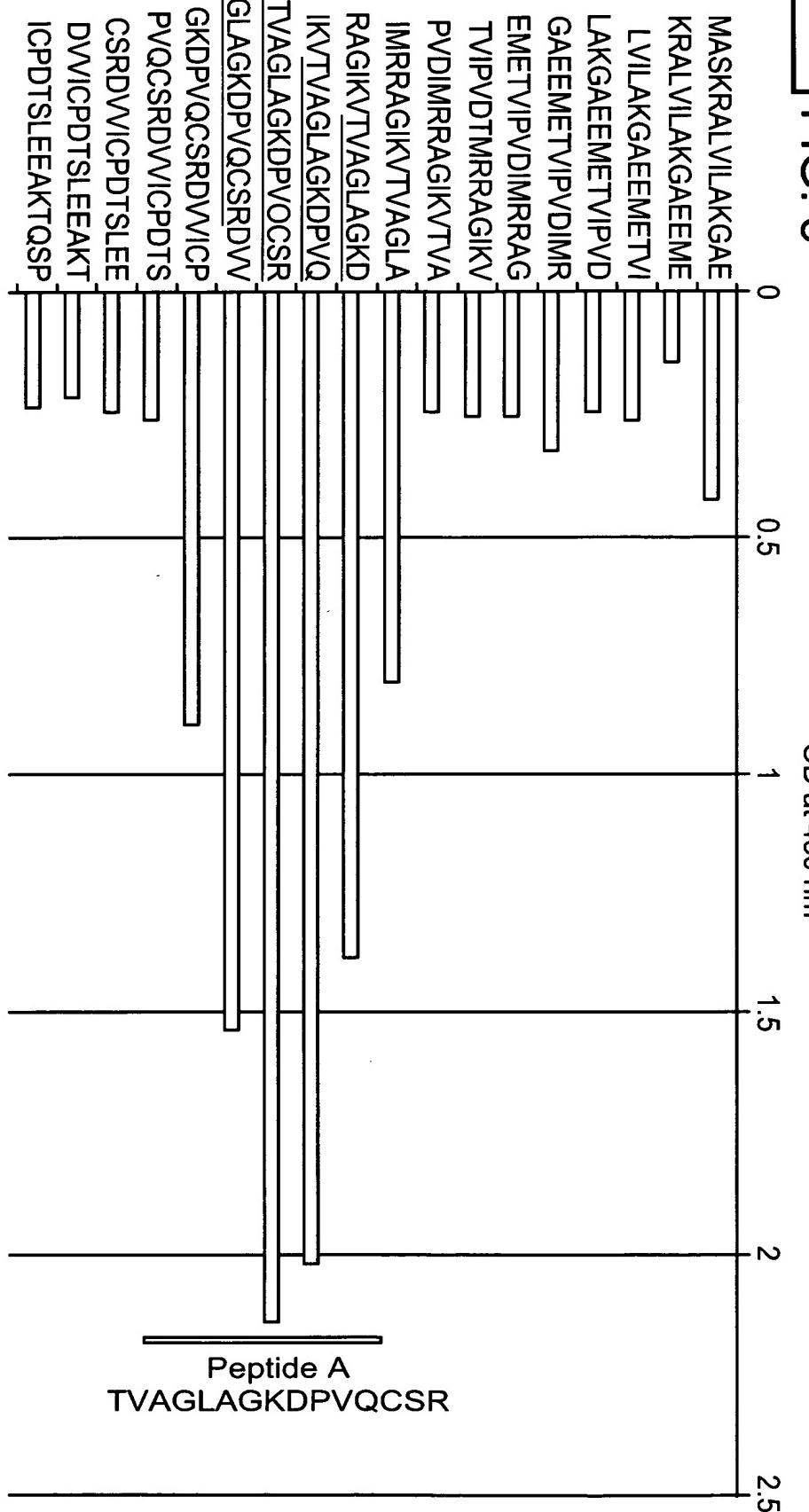


FIG. 8-1

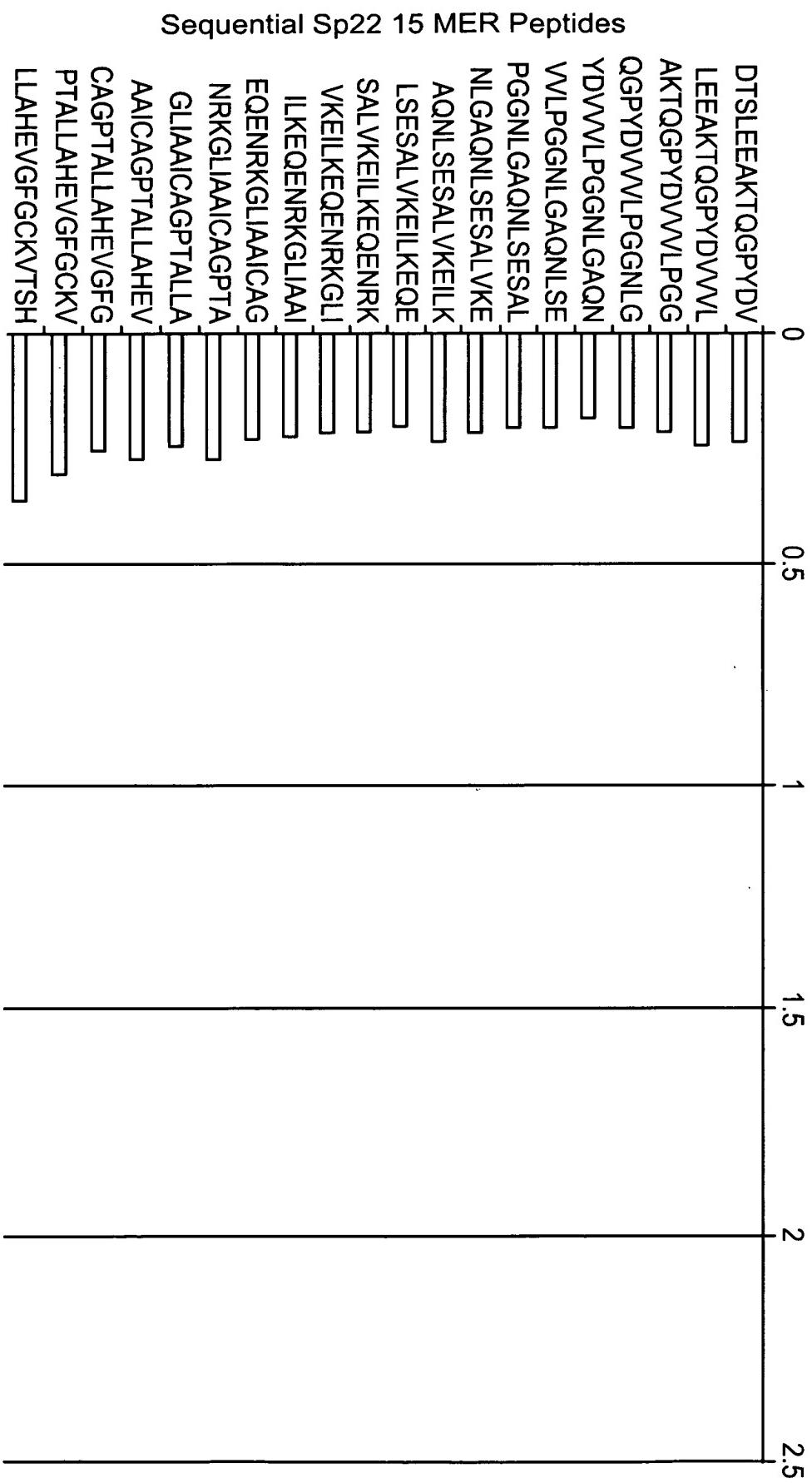


FIG. 8-2

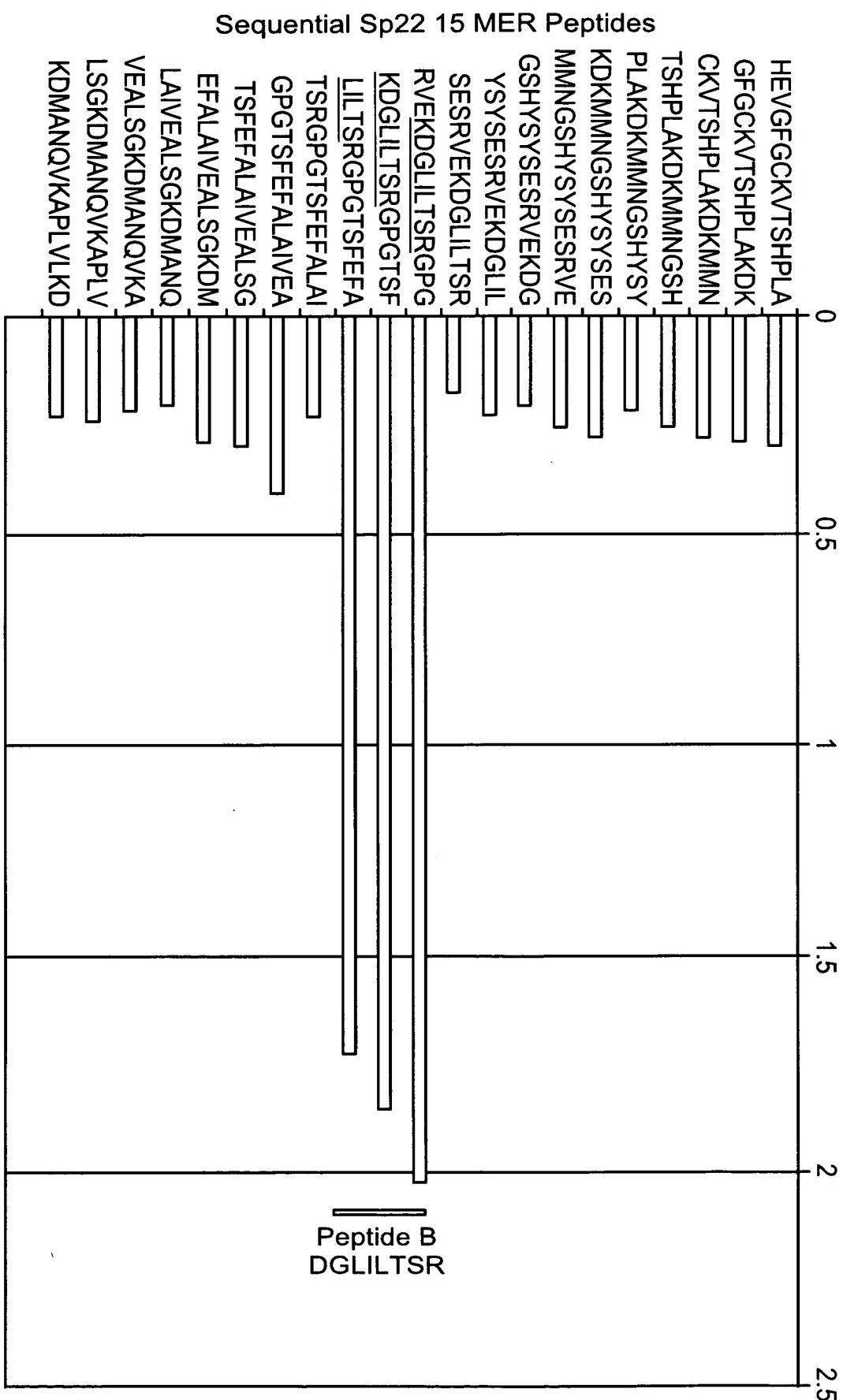
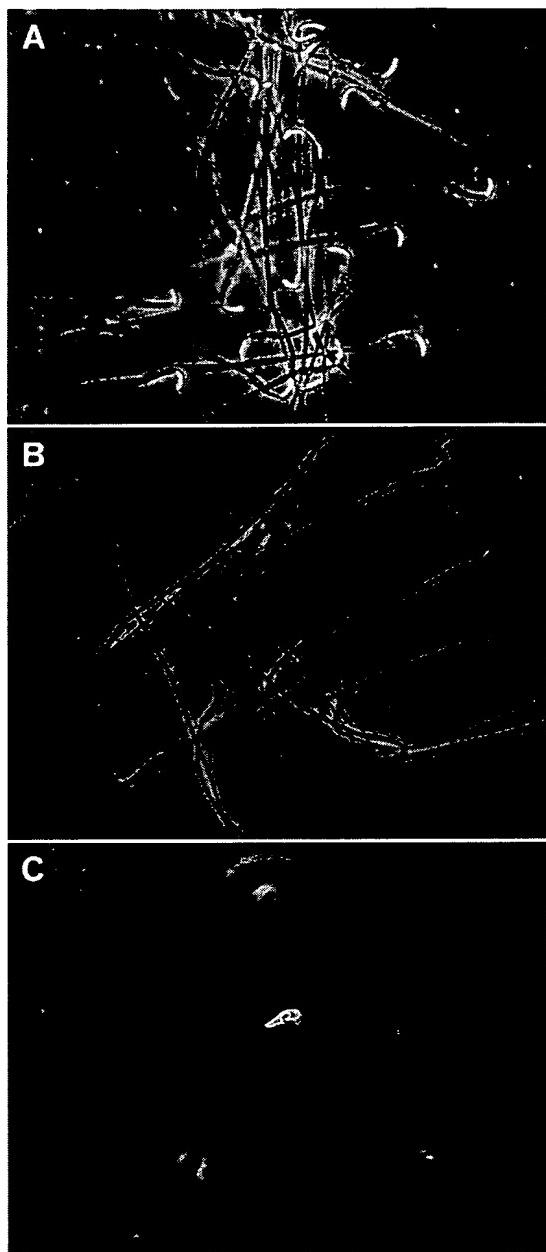


FIG. 8-3

**Fig. 9**



**Fig. 10**

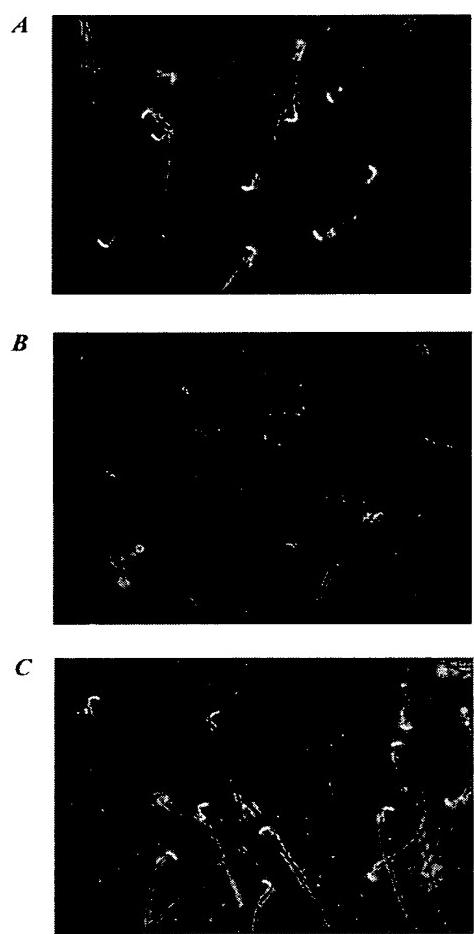
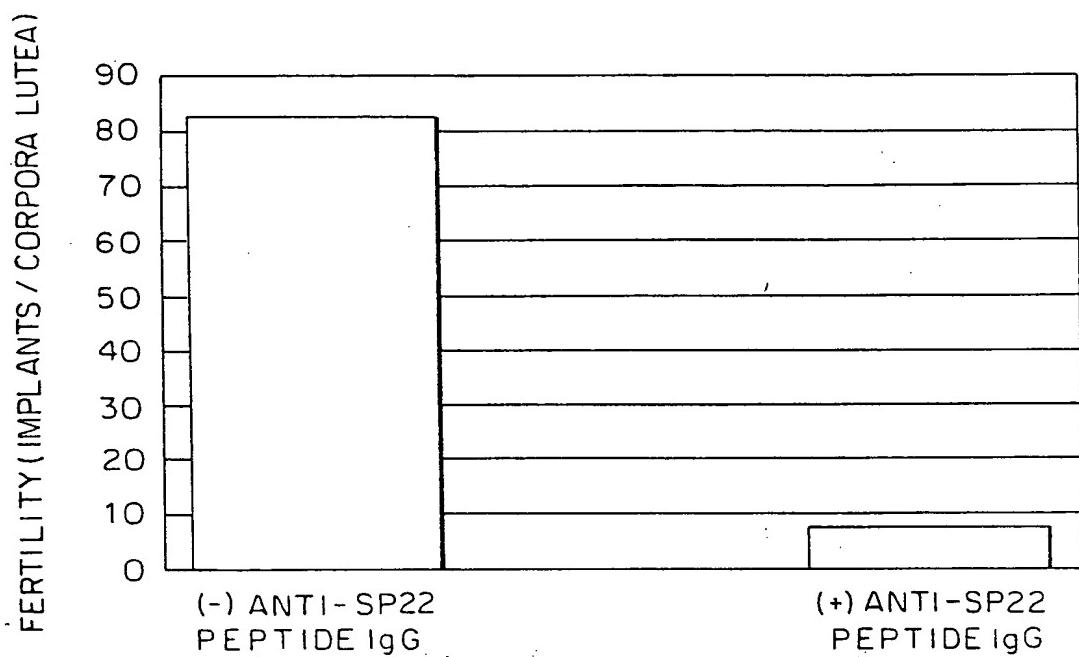


FIG. 11



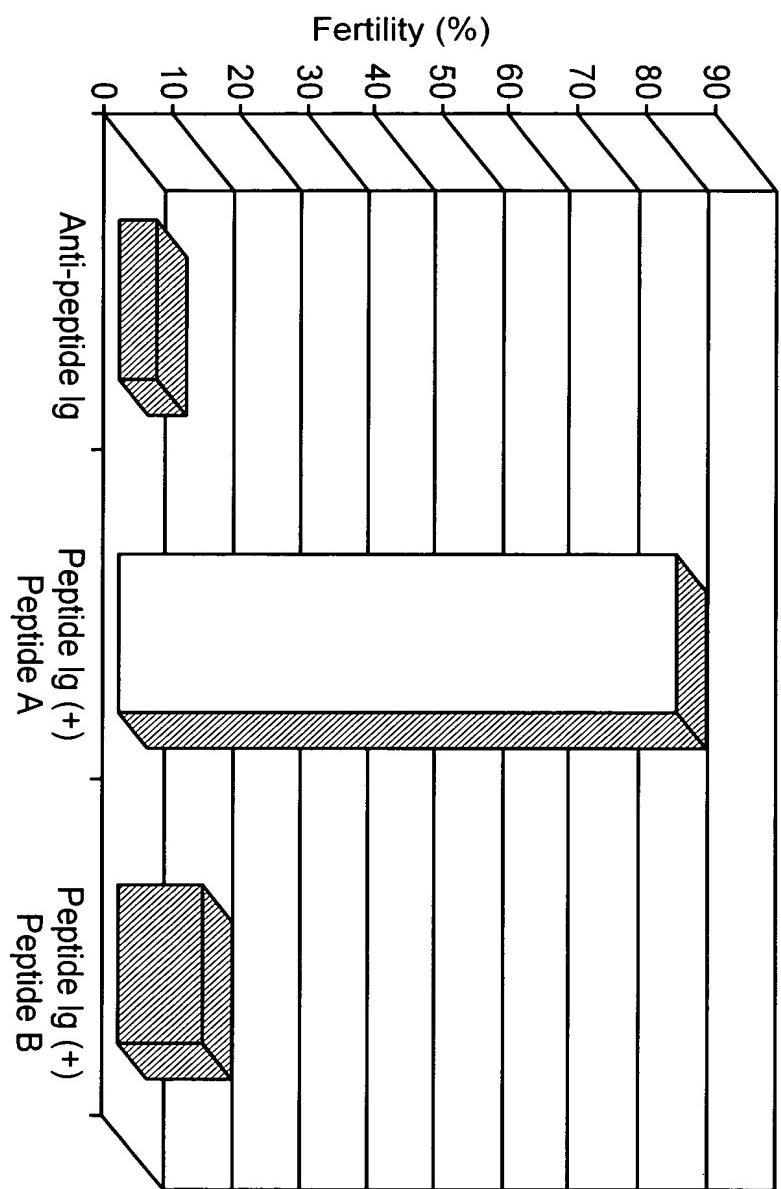


FIG. 12

**FIG. 13-1**

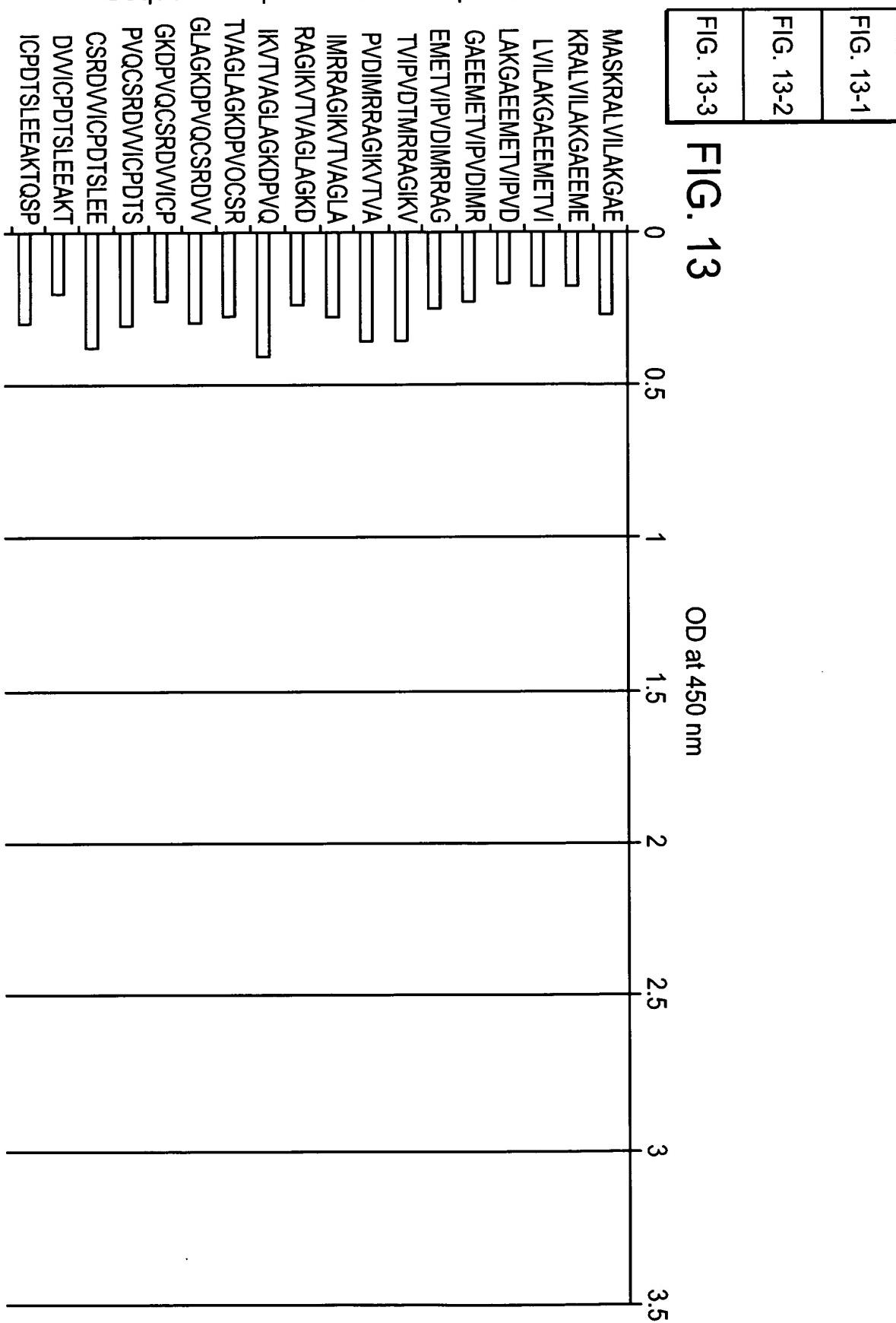
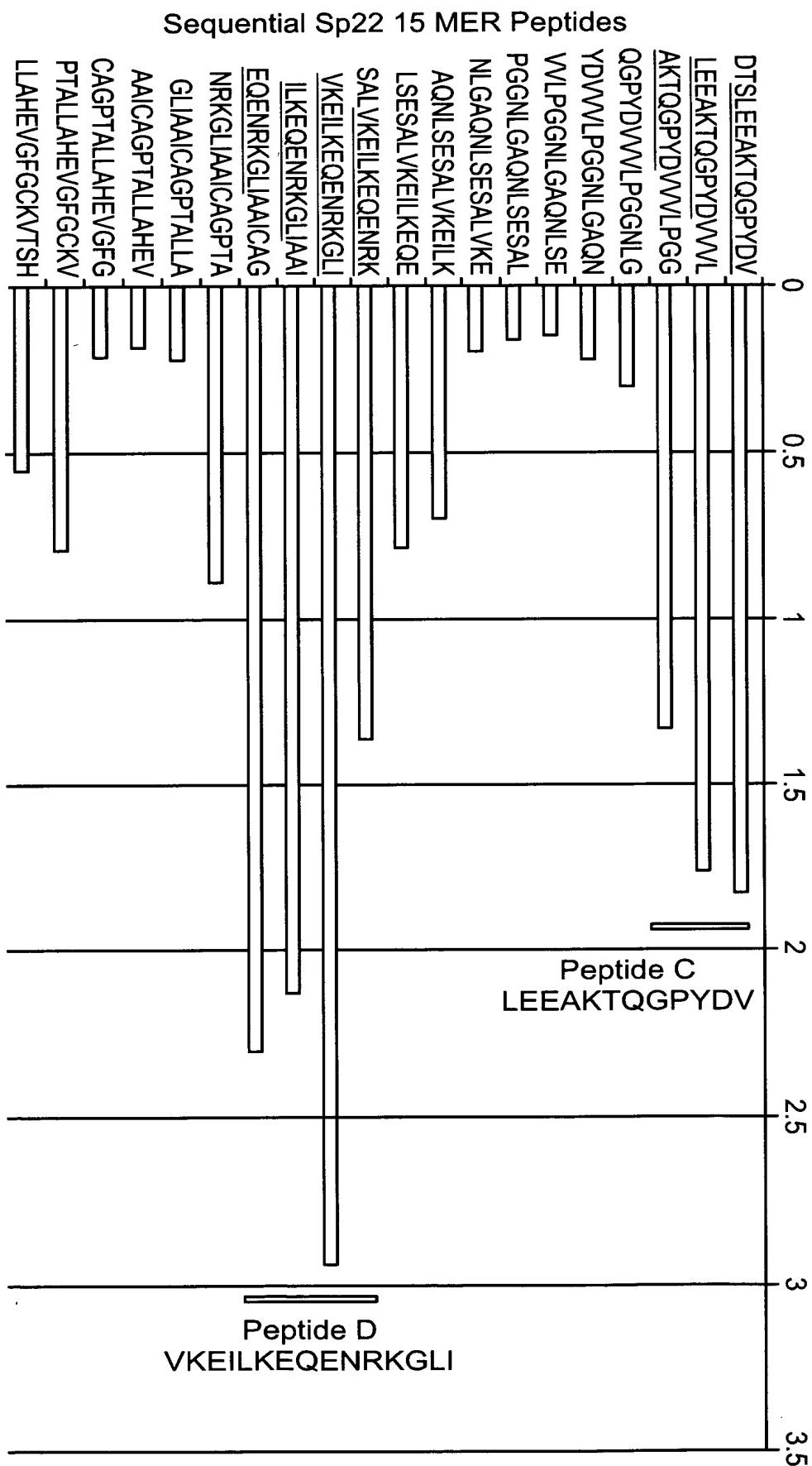


FIG. 13-2



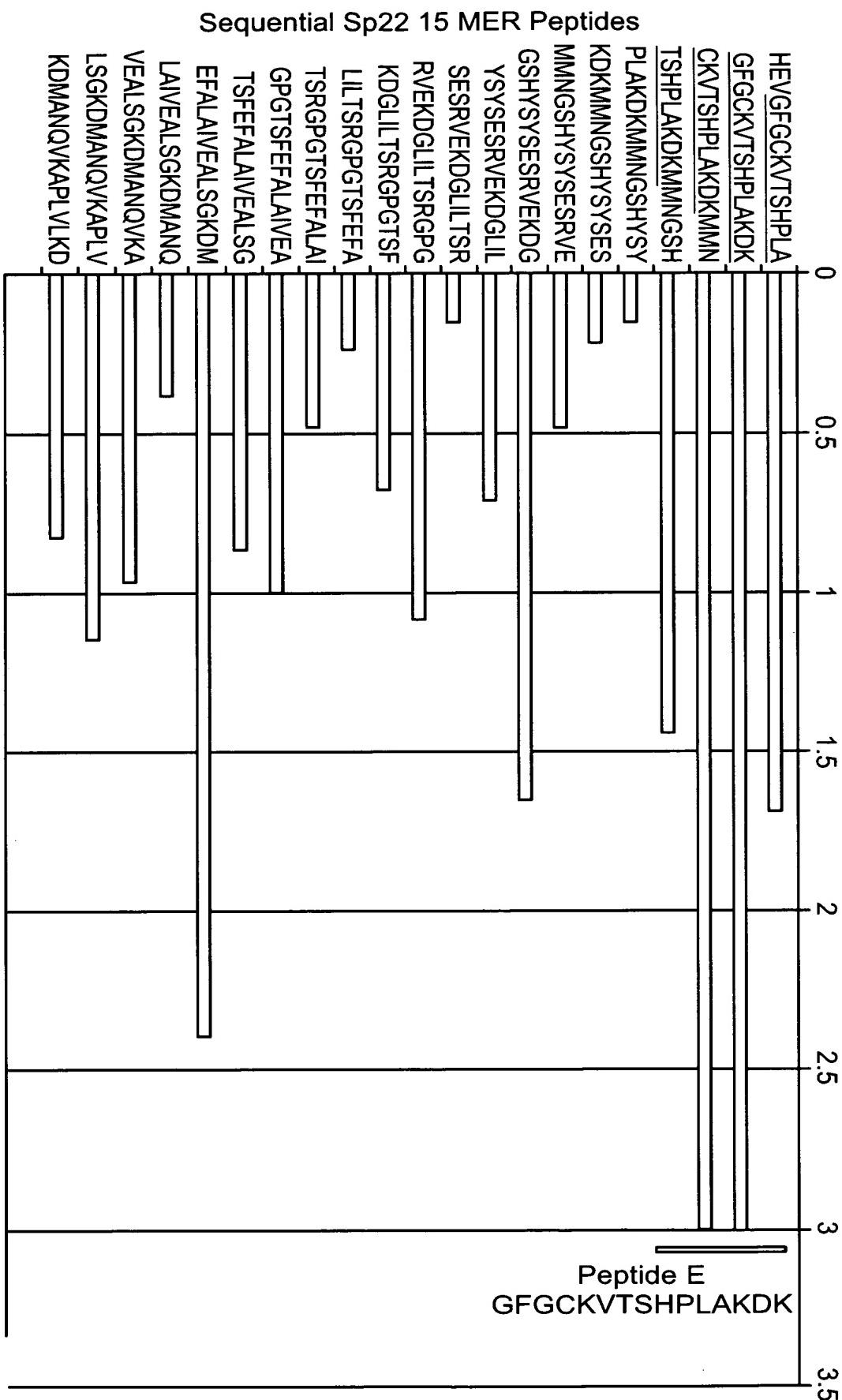


FIG. 13-3

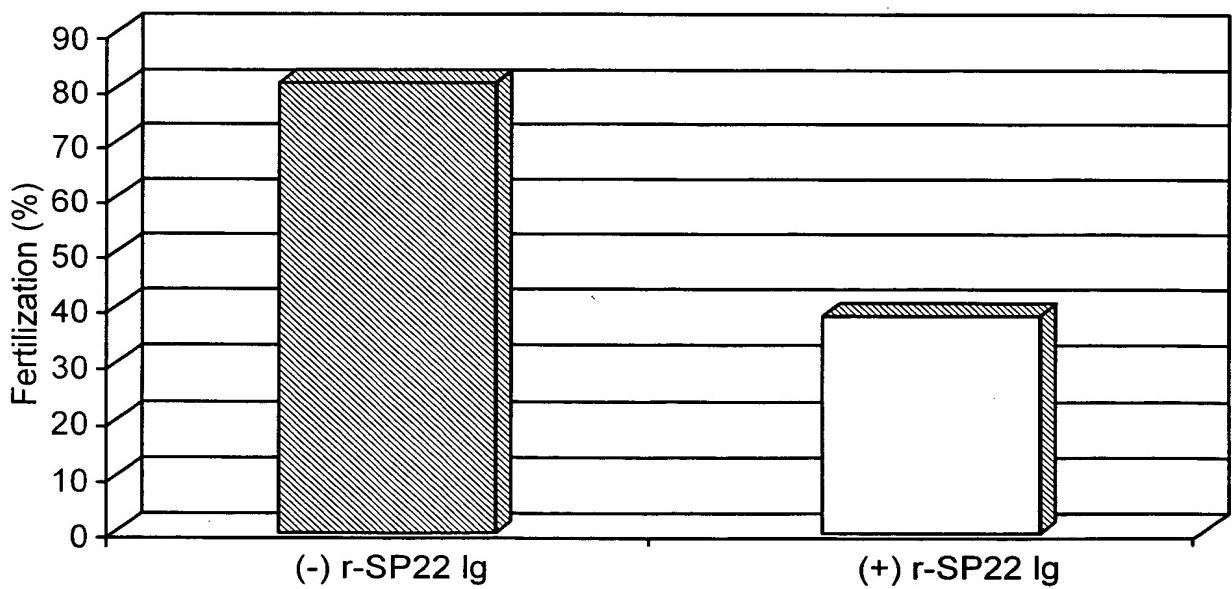
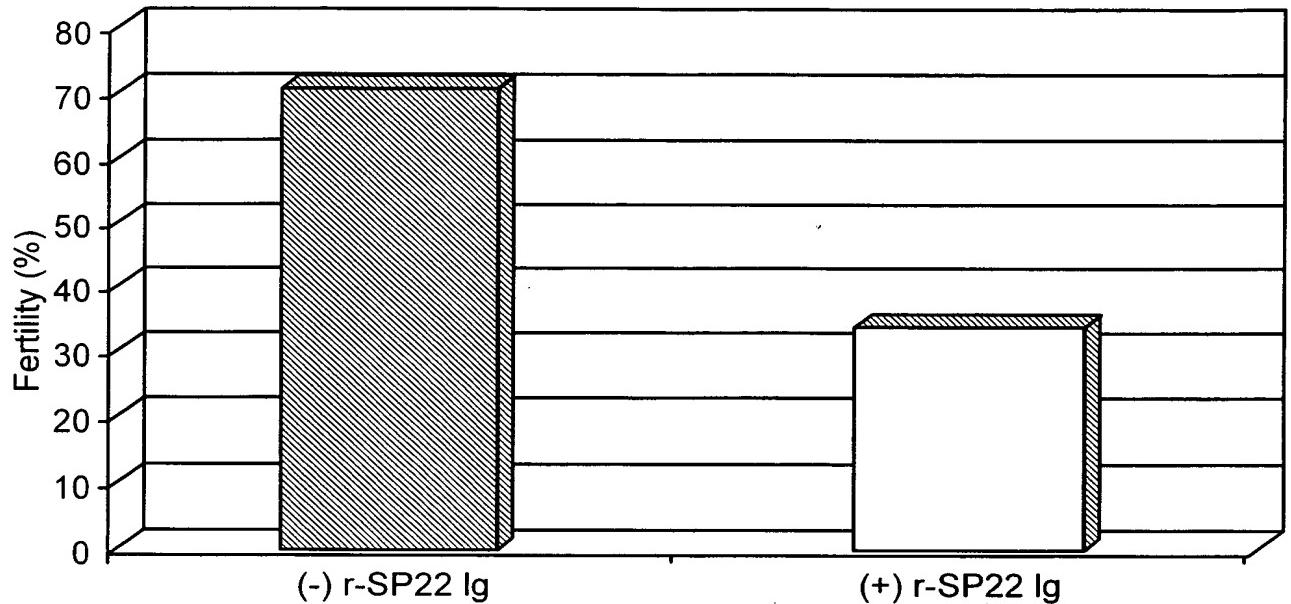


FIG. 14

FIG. 15

1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxatggcatccaaaagagctctggtcatc 66  
1 X X X X X X X X X X X X M A S K R A L V I 22  
67 ctagccaaaggagcagaggagatggagacagtgattcctgtggacatcatgcggcgagctgggatt 132  
23 L A K G A E E M E T V I P V D I M R R A G I 44  
133 aaagtccaccgttgcaggcttggctggaaaggaccccgtgcagtgtagccgtatgtatgtatgt 198  
45 K V T V A G L A G K D P V Q C S R D V V I C 66  
199 ccggataccagtctggaagaagcaaaaacacagggaccatacgtatgtggttttccaggagga 264  
67 P D T S L E E A K T Q G P Y D V V V L P G G 88  
265 aatctgggtgcacagaacttatctgagtcggcttggtgaaggagatcctaaggagcaggagaac 330  
89 N L G A Q N L S E S A L V K E I L K E Q E N 110  
331 aggaagggcctcatagctgccatctgtgcgggtcctacggccctgctggctcacgaagttaggctt 396  
111 R K G L I A A I C A G P T A L L A H E V G F 132  
397 ggatgcaagggttacatcgcacccattggctaaggacaaaatgatgaacggcagtcactacagctac 462  
133 G C K V T S H P L A K D K M M N G S H Y S Y 154  
463 tcagagagccgtgtggagaaggacggcctcatcctcaccagccgtggcctggaccagcttcgag 528  
155 S E S R V E K D G L I L T S R G P G T S F E 176  
528 ttgcgcgtggccattgtggaggcactcagtggcaaggacatggctaaccaaagtgaaggccccgctt 594  
177 F A L A I V E A L S G K D M A N Q V K A P L 198  
595 gttctcaaagactagagagcccaagccctggaccctggaccccccaggctgagcaggcatttggaaagc 660  
199 V L K D \* 202  
661 ccactagagagaccacagccagtgaacctggcatttggaaaggccactagtggtccacagccagt 726  
727 gaacctcaggaactaacgtgtgaagttagccgcgtcaggaatctcgccctggctctgtactatt 792  
793 ctgagcccttgcgttagataataacagttccccaaqctc 830

FIG. 16

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1      gctgtgcagagccgtctggcagggttacccctaaaggatattccatcttattaatcattag 65
66     tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatccagcagttta 130
131    tcggaacagcaacaacagcaacaaaaccttcaaaattacaagtcttaagaaaatagaaATGgca 195
1                                M A 2
196    tccaaaagagctctggtcatcctagccaaaggagcagaggagatggagacagtgattcctgtgga 260
3          S K R A L V I L A K G A E E M E T V I P V D 24
261    caccatgcggcgagctgggattaaagtaccgttgcaggctggctggaaaggaccccgtgcagt 325
25          I M R R A G I K V T V A G L A G K D P V Q 45
326    gtagccgtgatgttagtgatttgcggataccagtctggaaagaagcaaaaacacagggaccatac 390
46          C S R D V V I C P D T S L E E A K T Q G P Y 67
391    gatgtggttgttcttccaggagggaaatctgggtgcacagaacttatctgagtcggcttggtaa 455
68          D V V V L P G G N L G A Q N L S E S A L V K 89
456    ggagatcctcaaggagcaggagaacaggaaggccctcatagctgccatctgtgcgggtccacgg 520
90          E I L K E Q E N R K G L I A A I C A G P T 110
521    ccctgctggctcacgaagttaggcttggatgcaaggttacatcgcacccattggctaaggacaaa 585
111    A L L A F E V G F G C K V T S H P L A K D K 132
586    atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggccctcatcctcac 650
133    M M N G S H Y S Y S E S R V E K D G L I L T 154
651    cagccgtggccctgggaccagcttcgagttgcgtggccattgtggaggcactcagtgccaagg 715
155    S R G P G T S F E F A L A I V E A L S G K 175
716    acatggctaaccaaagtgaaggcccccttgcattcaaagacTAGagagcccaagccctggaccct 780
176    D M A N Q V K A P L V L K D 189
781    ggaccccccaggctgagcaggcattggaagcccactagtggtccacagcccaagtgaacccat 845
846    tggaagcccactagtgtgtccacagcccaagtgaacccatcaggaactaacgtgtgaagttagccgct 910
911    gctcaggaatctcgccctggctctgtactattctgagccctgcttagtagaataaacagttcccc 975

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